

AMENDMENTS TO THE CLAIMS, COMPLETE LISTING OF CLAIMS
IN ASCENDING ORDER WITH STATUS INDICATOR

Please amend the following claims as indicated.

1. (Currently Amended) A method for determining amino acid sequence of a peptide, comprising the steps of:

preparing an amino acid derivative, said amino acid derivative being negatively charged as a whole molecule and comprising an amino acid having an amino group protected with a protective group and a side chain containing an acidic group;

preparing a peptide of interest or fragments thereof obtained by optionally cleaving the peptide of interest for coupling to said amino acid derivative;

coupling an said amino acid derivative to the N-terminus of the peptide of interest or the fragments thereof, the amino acid derivative having protected an amino group with a protective group and derived from an amino acid with a side chain containing an acidic group to obtain a coupled peptide molecule; and

subjecting the coupled product peptide molecule to mass spectrometry analysis, wherein the analysis of the mass spectra of the peptide molecule determines the amino acid sequence of the peptide.

2. (Original) The method according to claim 1, wherein the acidic group is selected from the group consisting of carboxyl, sulfo, phosphono, sulfate, and phosphate group.

3. (Original) The method according to claim 1, wherein the amino acid is selected from the group consisting of cysteic acid, aspartic acid, glutamic acid, threonine phosphate, serine phosphate, tyrosine sulfate, and tyrosine phosphate.

4. (Original) The method according to claim 1, wherein the protective group is a functional group other than a basic group.

5. (Original) The method according to claim 1, wherein the protective group is selected from the group consisting of biotinyl, acetyl, formyl, and phenylisothiocarbamyl.
6. (Original) The method according to claim 1, wherein the protective group is biotinyl.
7. (Original) The method according to claim 1, wherein the amino acid derivative is N-biotinylcysteic acid.
8. (Currently Amended) The method according to claim 1, wherein the cleaving peptide of interest is performed cleaved by using an enzyme that can specifically hydrolyze a peptide bond on the a C-terminal side of a basic amino acid residue.
9. (Currently Amended) The method according to claim 1, wherein the coupled peptide molecule or the peptide fragment coupled to the amino acid derivative is ionized and is decayed into decay ions, which are then subjected to mass spectrometry for separation and detection.
10. (Currently Amended) The method according to claim 9, wherein the coupled peptide molecule or the peptide fragment coupled to the amino acid derivative is ionized by matrix-assisted laser desorption ionization (MALDI).
11. (Original) The method according to claim 9, wherein the ions are separated and detected by time-of-flight mass spectrometry (TOFMS).